



SEQUENCE LISTING

<110> Cohen, Bruce D.  
Bedian, Vahe  
Obrocea, Mihail  
Gomez-Navarro, Jesus  
Cusmano, John D.  
Wang, Huifen F.  
Page, Kelly L.  
Guyot, Deborah J.

<120> USES OF ANTI-INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
ANTIBODIES

<130> PC25232A

<140>

<141>

<160> 60

<170> PatentIn Ver. 2.1

<210> 1

<211> 291

<212> DNA

<213> Homo sapiens

<400> 1

tgcacatctgta ggagacagag tcaccttcac ttgccgggca agtcaggaca ttagacgtga 60  
tttaggctgg tatcagcaga aaccagggaa agctcctaag cgcctgatct atgctgcac 120  
ccgtttacaa agtgggggtcc catcaagggt cagcggcagt ggatctggga cagaattcac 180  
tctcacaatc agcagcctgc agcctgaaga ttttgcaact tattactgtc tacagcataa 240  
taattatcct cggacgttcg gccaaaggac cgaggtggaa atcatacgaa c 291

<210> 2

<211> 136

<212> PRT

<213> Homo sapiens

<400> 2

Ala Ser Val Gly Asp Arg Val Thr Phe Thr Cys Arg Ala Ser Gln Asp  
1 5 10 15

Ile Arg Arg Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro  
20 25 30

Lys Arg Leu Ile Tyr Ala Ala Ser Arg Leu Gln Ser Gly Val Pro Ser  
 35 40 45

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser  
 50 55 60

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn  
 65 70 75 80

Asn Tyr Pro Arg Thr Phe Gly Gln Gly Thr Glu Val Glu Ile Ile Arg  
 85 90 95

Thr Val Ala Ala'Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
 100 105 110

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
 115 120 125

Pro Arg Glu Ala Lys Val Gln Trp  
 130 135

<210> 3  
 <211> 352  
 <212> DNA  
 <213> Homo sapiens

<400> 3  
 gggaggcttg gtcaagcctg gaggtccctg agactctcct gtgcagcctc tggattcact 60  
 ttcagtgact actatatgag ctggatccgc caggctccag ggaaggggct ggaatggggt 120  
 tcatacatta gtagtagtgg tagtaccaga gactacgcag actctgtgaa gggccgattc 180  
 accatctcca gggacaacgc caagaactca ctgtatctgc aaatgaacag cctgagagcc 240  
 gaggacacgg ccgtgtatta ctgtgtgaga gatggagtgg aaactacttt ttactactac 300  
 tactacggta tggacgtctg gggccaaggg accacgggtca ccgtctcctc ag 352

<210> 4  
 <211> 174  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
 Gly Arg Leu Gly Gln Ala Trp Arg Ser Leu Arg Leu Ser Cys Ala Ala  
 1 5 10 15

Ser Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ser Trp Ile Arg Gln Ala  
 20 25 30

Pro Gly Lys Gly Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Gly Ser  
           35                          40                          45  
 Thr Arg Asp Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg  
           50                          55                          60  
 Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala  
           65                          70                          75                          80  
 Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg Asp Gly Val Glu Thr Thr  
                           85                          90                          95  
 Phe Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr  
                           100                          105                          110  
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
           115                          120                          125  
 Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys  
           130                          135                          140  
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
           145                          150                          155                          160  
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ser Cys Ala  
                           165                          170

<210> 5  
 <211> 322  
 <212> DNA  
 <213> Homo sapiens

<400> 5  
 gacatccaga tgacccagtt tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
 atcacttgcc gggcaagtca gggcattaga aatgatttag gctggatatca gcagaaacca 120  
 gggaaagccc ctaagcgct gatctatgct gcatcccggt tgcacagagg ggtcccatca 180  
 aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240  
 gaagattttg caacttatta ctgtttacaa cataatagtt acccgtgcag ttttggccag 300  
 gggaccaagc tggagatcaa ac 322

<210> 6  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 6

Asp Ile Gln Met Thr Gln Phe Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp  
 20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile  
 35 40 45

Tyr Ala Ala Ser Arg Leu His Arg Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Cys  
 85 90 95

Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
 100 105

<210> 7  
 <211> 375  
 <212> DNA  
 <213> Homo sapiens

<400> 7  
 aggtgcagct gttggagtct gggggaggct tgggtacagcc tgggggggtcc ctgagactct 60  
 cctgtacagc ctctggattc accttttagca gctatgccat gaactgggtc cgccaggctc 120  
 caggaagg gctggagtgg gtctcagcta ttagtggttag tgggtggtacc acattctacg 180  
 cagactccgt gaagggccgg ttcaccatct ccagagacaa ttccaggacc acgctgtatc 240  
 tgcaaagtga cagcctgaga gccgaggaca cggccgtata ttactgtgcg aaagatcttg 300  
 gctggtccga ctcttactac tactactacg gtatggacgt ctggggccaa gggaccacgg 360  
 tcaccgtctc ctacg 375

<210> 8  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
 Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser  
 1 5 10 15

Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala  
 20 25 30

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser  
 35 40 45

Ala Ile Ser Gly Ser Gly Gly Thr Thr Phe Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Thr Thr Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Lys Asp Leu Gly Trp Ser Asp Ser Tyr Tyr Tyr Tyr Tyr Gly Met Asp  
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
 115 120

<210> 9  
 <211> 302  
 <212> DNA  
 <213> Homo sapiens

<400> 9  
 tcctccctgt ctgcatctgt aggagacaga gtcaccttca cttgccgggc aagtcaggac 60  
 attagacgtg atttaggctg gtatcagcag aaaccaggga aagctcctaa gcgcctgac 120  
 tatgctgcat cccgtttaca aagtggggtc ccatcaagggt tcagcggcag tggatctggg 180  
 acagaattca ctctcacaat cagcagcctg cagcctgaag attttgcaac ttattactgt 240  
 ctacagcata ataattatcc tcggacgttc ggccaaggga ccgaggtgga aatcatacga 300  
 ac 302

<210> 10  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 10  
 Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Phe Thr Cys Arg  
 1 5 10 15

Ala Ser Gln Asp Ile Arg Arg Asp Leu Gly Trp Tyr Gln Gln Lys Pro  
 20 25 30

Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Arg Leu Gln Ser  
 35 40 45

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr  
 50 55 60

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys  
 65 70 75 80

Leu Gln His Asn Asn Tyr Pro Arg Thr Phe Gly Gln Gly Thr Glu Val  
 85 90 95

Glu Ile Ile Arg  
 100

<210> 11

<211> 338

<212> DNA

<213> Homo sapiens

<400> 11

gggccaggga ctggtgaagc cttcggagac cctgtccctc acctgcactg tctctgggtgg 60  
 ctccatcagt aattactact ggagctggat ccggcagccc gccgggaagg gactggagtg 120  
 gattggggcgt atctatacca gtgggagccc caactacaac ccctccctca agagtcgagt 180  
 caccatgtca gtagacacgt ccaagaacca gttctccctg aagctgaact ctgtgaccgc 240  
 cgcggaacac gccgtgtatt actgtgcggt aacgattttt ggagtgggta ttatctttga 300  
 ctactggggc cagggaaccc tggtcaccgt ctccctcag 338

<210> 12

<211> 112

<212> PRT

<213> Homo sapiens

<400> 12

Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr  
 1 5 10 15

Val Ser Gly Gly Ser Ile Ser Asn Tyr Tyr Trp Ser Trp Ile Arg Gln  
 20 25 30

Pro Ala Gly Lys Gly Leu Glu Trp Ile Gly Arg Ile Tyr Thr Ser Gly  
 35 40 45

Ser Pro Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Ser Val  
 50 55 60

Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Asn Ser Val Thr Ala  
 65 70 75 80

Ala Asp Thr Ala Val Tyr Tyr Cys Ala Val Thr Ile Phe Gly Val Val  
85 90 95

Ile Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
100 105 110

<210> 13  
<211> 322  
<212> DNA  
<213> Homo sapiens

<400> 13  
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gggcattaga agtgatttag gctggtttca gcagaaacca 120  
gggaaagccc ctaagcgcct gatctatgct gcatccaaat tacaccgtgg ggtcccatca 180  
aggttcagcg gcagtggatc tgggacagaa ttcaactetca caatcagccg cctgcagcct 240  
gaagattttg caacttatta ctgtctacag cataatagtt accctctcac tttcggcgga 300  
gggaccaagg tggagatcaa ac 322

<210> 14  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 14  
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Ser Asp  
20 25 30  
Leu Gly Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile  
35 40 45  
Tyr Ala Ala Ser Lys Leu His Arg Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60  
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Arg Leu Gln Pro  
65 70 75 80  
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu  
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 100 105

<210> 15  
 <211> 376  
 <212> DNA  
 <213> Homo sapiens

<400> 15  
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60  
 tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120  
 ccaggaagg ggctggagt ggtctcagct attagtggta gtggtggtat cacatactac 180  
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240  
 ctgcaaata acagcctgag agccgaggac acggccgtat attactgtgc gaaagatctg 300  
 ggctacggtg acttttacta ctactactac ggtatggacg tctggggcca agggaccacg 360  
 gtcaccgtct cctcag 376

<210> 16  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 20 25 30  
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Ala Ile Ser Gly Ser Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Lys Asp Leu Gly Tyr Gly Asp Phe Tyr Tyr Tyr Tyr Tyr Gly Met  
 100 105 110  
 Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser



115

120

125

&lt;210&gt; 17

&lt;211&gt; 279

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

caggagacag agtcaccatc acttgccggg caagtcagag cattagtacc tttttaaatt 60  
 ggtatcagca gaaaccaggg aaagccccta aactcctgat ccatgttgca tccagtttac 120  
 aaggtgggggt cccatcaagg ttcagtggca gtggatctgg gacagatttc actctcacca 180  
 tcagcagtct gcaacctgaa gattttgcaa cttactactg tcaacagagt tacaatgccc 240  
 cactcacttt cggcggaggg accaaggtgg agatcaaac 279

&lt;210&gt; 18

&lt;211&gt; 92

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 18

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr  
 1 5 10 15

Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu  
 20 25 30

Ile His Val Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser  
 35 40 45

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln  
 50 55 60

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asn Ala Pro  
 65 70 75 80

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 85 90

&lt;210&gt; 19

&lt;211&gt; 341

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

cccaggactg gtgaagcctt cggagaccct gtccctcacc tgcactgtct ctgggtggctc 60

catcagtagt tactactgga gttggatccg gcagcccccac gggaagggac tggagtggat 120  
 tgggtatatc tattacagtg ggagcaccaa ctacaacccc tccctcaaga gtcgagtcac 180  
 catatcagta gacacgtcca agaaccagtt ctccctgaag ctgagttctg tgaccgctgc 240  
 ggacacggcc gtgtattact gtgccaggac gtatagcagt tcgttctact actacggtat 300  
 ggacgtctgg ggccaaggga ccacggtcac cgtctcctca g 341

<210> 20

<211> 113

<212> PRT

<213> Homo sapiens

<400> 20

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val  
 1 5 10 15

Ser Gly Gly Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro  
 20 25 30

Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser  
 35 40 45

Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp  
 50 55 60

Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala  
 65 70 75 80

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Thr Tyr Ser Ser Ser Phe Tyr  
 85 90 95

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser  
 100 105 110

Ser

<210> 21

<211> 274

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (240)

<223> a, c, t, g, other or unknown

<400> 21  
agagccaccc tctcctgtag ggccagtcag agtggtcgcg gcaggtactt agcctgggtac 60  
cagcagaaac ctggccaggc tcccaggctc ctcatctatg gtgcatccag cagggccact 120  
ggcatcccag acagggttcag tggcagtggg tctgggacag acttcactct caccatcagc 180  
agactggagc ctgaagattt tgcagtgttt tactgtcagc agtatggtag ttcacctcgn 240  
acgttcggcc aagggaacaa ggtggaaatc aaac 274

<210> 22  
<211> 91  
<212> PRT  
<213> Homo sapiens

<400> 22  
Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Gly Arg Tyr  
1 5 10 15  
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
20 25 30  
Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly  
35 40 45  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro  
50 55 60  
Glu Asp Phe Ala Val Phe Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Arg  
65 70 75 80  
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
85 90

<210> 23  
<211> 367  
<212> DNA  
<213> Homo sapiens

<400> 23  
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60  
tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120  
ccagggaagg ggctggagtg ggtctcaggt attactggga gtggtggtag tacatactac 180  
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240  
ctgcaaataa acagcctgag agccgaggac acggccgtat attactgtgc gaaagatcca 300  
gggactacgg tgattatgag ttggttcgac ccctggggcc aggggaaccct ggtcaccgtc 360  
tcctcag 367

<210> 24  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 20 25 30  
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gly Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Lys Asp Pro Gly Thr Thr Val Ile Met Ser Trp Phe Asp Pro Trp  
 100 105 110  
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 115 120

<210> 25  
 <211> 320  
 <212> DNA  
 <213> Homo sapiens

<400> 25  
 gaactgtggc tgcaccatct gtcttcacat tcccgccatc tgatgagcag ttgaaatctg 60  
 gaactgcctc tggtgtgtgc ctgctgaata acttctatcc cagagaggcc aaagtacagt 120  
 ggaaggtgga taacgcctc caatcgggta actcccagga gagtgtcaca gagcaggaca 180  
 gcaaggacag cacctacagc ctcagcagca ccctgacgct gagcaaagca gactacgaga 240  
 aacacaaagt ctacgcctgc gaagtcaccc atcagggcct gagctcgccc gtcacaaaga 300  
 gcttcaacag gggagagtgt 320

<210> 26  
 <211> 106  
 <212> PRT

<213> Homo sapiens

<400> 26

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
1 5 10 15  
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
20 25 30  
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
35 40 45  
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
50 55 60  
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
65 70 75 80  
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
85 90 95  
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
100 105

<210> 27

<211> 978

<212> DNA

<213> Homo sapiens

<400> 27

gcctccacca agggcccac t ggtcttcccc ctggcgccct gctccaggag cacctccgag 60  
agcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 120  
tggaactcag gcgctctgac cagcggcgctg cacaccttcc cagctgtcct acagtcctca 180  
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcaacttcgg caccagacc 240  
tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagac agttgagcgc 300  
aaatgttgtg tcgagtgcc accgtgcca gcaccacctg tggcaggacc gtcagtcttc 360  
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacgtgc 420  
gtgggtgggtg acgtgagcca cgaagacccc gaggtccagt tcaactggta cgtggacggc 480  
gtggaggtgc ataatgccaa gacaaagcca cgggaggagc agttcaacag cacgttccgt 540  
gtggtcagcg tcctcaccgt tgtgcaccag gactggctga acggcaagga gtacaagtgc 600  
aaggtctcca acaaaggcct ccagcccc atcgagaaaa ccatctccaa aaccaaagg 660  
cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac 720  
caggtcagcc tgacctgcct ggtcaaaggc ttctaccca gcgacatcgc cgtggagtgg 780  
gagagcaatg ggcagccgga gaacaactac aagaccacac ctcccatgct ggactccgac 840  
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 900  
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 960  
tcctgtctc cggtgtaa 978

<210> 28

<211> 326

<212> PRT

<213> Homo sapiens

<400> 28

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr  
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys  
85 90 95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
100 105 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
115 120 125

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
130 135 140

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly  
145 150 155 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn  
165 170 175

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp  
180 185 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro  
195 200 205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu

210	215	220
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn		
225	230	235 240
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile		
	245	250 255
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr		
	260	265 270
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys		
	275	280 285
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys		
	290	295 300
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu		
305	310	315 320
Ser Leu Ser Pro Gly Lys		
	325	

<210> 29  
 <211> 296  
 <212> DNA  
 <213> Homo sapiens

<400> 29  
 caggtgcagc tgggtggagtc tggggggaggc ttggtcaagc ctggaggggtc cctgagactc 60  
 tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120  
 ccaggggaagg ggctggagtg ggtttcatac attagtagta gtggtagtag catatactac 180  
 gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagaa ctcactgtat 240  
 ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagaga 296

<210> 30  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 30  
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr  
 20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg

<210> 31  
 <211> 296  
 <212> DNA  
 <213> Homo sapiens

<400> 31  
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60  
 tcctgtgcag cctctggatt caccttttagc agctatgccca tgagctgggt ccgccaggct 120  
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggttag cacatactac 180  
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240  
 ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaga 296

<210> 32  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 32  
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60



Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys

<210> 33  
<211> 296  
<212> DNA  
<213> Homo sapiens

<400> 33  
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggggac cctgtccctc 60  
acctgcgctg tctctggtgg ctccatcagc agtagtaact ggtggagttg ggtccgccag 120  
ccccagggga aggggctgga gtggattggg gaaatctatc atagtgggag caccaactac 180  
aaccctgcc tcaagagtcg agtcaccata tcagtagaca agtccaagaa ccagttctcc 240  
ctgaagctga gctctgtgac cgccgcggac acggccgtgt attactgtgc gagaga 296

<210> 34  
<211> 98  
<212> PRT  
<213> Homo sapiens

<400> 34  
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser  
20 25 30

Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp  
35 40 45

Ile Gly Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu  
50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Lys Ser Lys Asn Gln Phe Ser  
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg

<210> 35  
 <211> 293  
 <212> DNA  
 <213> Homo sapiens

<400> 35  
 cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
 acctgcactg tctctggtgg ctccatcagt agttactact ggagctggat ccggcagccc 120  
 ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180  
 ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240  
 aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag aga 293

<210> 36  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 36  
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15  
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
 20 25 30  
 Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60  
 Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80  
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95  
 Arg

<210> 37  
 <211> 290  
 <212> DNA  
 <213> Homo sapiens

<400> 37  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtc gagtggttagc agcagctact tagcctggta ccagcagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gtcacctcc 290

<210> 38  
<211> 96  
<212> PRT  
<213> Homo sapiens

<400> 38  
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15  
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
20 25 30  
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45  
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60  
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80  
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

<210> 39  
<211> 288  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (288)  
<223> a, c, t, g, other or unknown

<400> 39

```

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120
gggaaagccc ctaagcgctt gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacag cataatagtt accctccn                288

```

<210> 40

<211> 96

<212> PRT

<213> Homo sapiens

<400> 40

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
  1                      5                      10                     15

```

```

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
          20                      25                     30

```

```

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
      35                      40                     45

```

```

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
      50                      55                     60

```

```

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
      65                      70                     75                     80

```

```

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro
          85                      90                     95

```

<210> 41

<211> 288

<212> DNA

<213> Homo sapiens

<400> 41

```

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagtcctt gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcch                288

```

<210> 42  
 <211> 96  
 <212> PRT  
 <213> Homo sapiens

<400> 42  
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr  
 20 25 30  
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro  
 85 90 95

<210> 43  
 <211> 293  
 <212> DNA  
 <213> Homo sapiens

<400> 43  
 cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
 acctgcactg tctctggtgg ctccatcagt agttactact ggagctggat ccggcagccc 120  
 gccgggaagg gactggagtg gattgggcgt atctatacca gtgggagcac caactacaac 180  
 cctccctca agagtcgagt caccatgtca gtagacacgt ccaagaacca gttctcctg 240  
 aagctgagct ctgtgaccgc cgcgacacg gccgtgtatt actgtgagc aga 293

<210> 44  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 44  
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1	5	10	15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr			
20	25	30	
Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile			
35	40	45	
Gly Arg Ile Tyr Thr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys			
50	55	60	
Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu			
65	70	75	80
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala			
85	90	95	

Arg

<210> 45  
 <211> 470  
 <212> PRT  
 <213> Homo sapiens

<400> 45
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1 5 10 15
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
20 25 30
Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe
35 40 45
Ser Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Thr Thr Phe Tyr Ala
65 70 75 80
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Thr
85 90 95
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Lys Asp Leu Gly Trp Ser Asp Ser Tyr Tyr Tyr Tyr  
 115 120 125

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
 130 135 140

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
 145 150 155 160

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 165 170 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 180 185 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 195 200 205

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr  
 210 215 220

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 225 230 235 240

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
 245 250 255

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
 260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 275 280 285

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly  
 290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn  
 305 310 315 320

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp  
 325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro  
 340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu  
 355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
 370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
 405 410 415

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
 420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
 435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
 450 455 460

Ser Leu Ser Pro Gly Lys  
 465 470

<210> 46

<211> 470

<212> PRT

<213> Homo sapiens

<400> 46

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly  
 1 5 10 15

Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln  
 20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
 35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala  
 65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn  
 85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val  
 100 105 110



Tyr Tyr Cys Ala Lys Gly Tyr Ser Ser Gly Trp Tyr Tyr Tyr Tyr Tyr  
115 120 125  
Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
130 135 140  
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
145 150 155 160  
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
165 170 175  
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
180 185 190  
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
195 200 205  
Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr  
210 215 220  
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys  
225 230 235 240  
Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
245 250 255  
Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
260 265 270  
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
275 280 285  
Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly  
290 295 300  
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn  
305 310 315 320  
Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp  
325 330 335  
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro  
340 345 350  
Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu  
355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
 370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
 405 410 415

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
 420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
 435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
 450 455 460

Ser Leu Ser Pro Gly Lys  
 465 470

<210> 47

<211> 236

<212> PRT

<213> Homo sapiens

<400> 47

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15

Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Phe Pro Ser Ser  
 20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
 35 40 45

Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys  
 50 55 60

Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Arg Leu His Arg Gly Val  
 65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr  
 85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln

100	105	110
His Asn Ser Tyr Pro Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile		
115	120	125
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp		
130	135	140
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn		
145	150	155
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu		
165	170	175
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp		
180	185	190
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr		
195	200	205
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser		
210	215	220
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys		
225	230	235

<210> 48

<211> 236

<212> PRT

<213> Homo sapiens

<400> 48

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp		
1	5	10
Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser		
20	25	30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser		
35	40	45
Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys		
50	55	60
Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val		
65	70	75
		80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr  
                             85                            90                            95  
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln  
                             100                            105                            110  
 His Asn Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile  
                             115                            120                            125  
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
                             130                            135                            140  
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
 145                            150                            155                            160  
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
                             165                            170                            175  
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
                             180                            185                            190  
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
                             195                            200                            205  
 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
                             210                            215                            220  
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225                            230                            235

<210> 49  
 <211> 470  
 <212> PRT  
 <213> Homo sapiens

<400> 49  
 Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Ile Lys Gly  
   1                            5                            10                            15  
 Val Gln Cys Gln Ala Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys  
                             20                            25                            30  
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
                             35                            40                            45  
 Ser Asp Tyr Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu  
                             50                            55                            60

Glu	Trp	Val	Ser	Tyr	Ile	Ser	Ser	Ser	Gly	Ser	Thr	Arg	Asp	Tyr	Ala	65	70	75	80
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	85	90	95	
Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	100	105	110	
Tyr	Tyr	Cys	Val	Arg	Asp	Gly	Val	Glu	Thr	Thr	Phe	Tyr	Tyr	Tyr	Tyr	115	120	125	
Tyr	Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	130	135	140	
Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	145	150	155	160
Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	165	170	175	
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	180	185	190	
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	195	200	205	
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Asn	Phe	Gly	Thr	Gln	Thr	210	215	220	
Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	225	230	235	240
Thr	Val	Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	245	250	255	
Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	260	265	270	
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	275	280	285	
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	290	295	300	
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	305	310	315	320

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp  
 325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro  
 340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu  
 355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
 370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
 405 410 415

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
 420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
 435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
 450 455 460

Ser Leu Ser Pro Gly Lys  
 465 470

<210> 50  
 <211> 473  
 <212> PRT  
 <213> Homo sapiens

<400> 50  
 Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Ile Lys Gly  
 1 5 10 15

Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys  
 20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
 35 40 45

Ser Asp Tyr Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu

50		55		60
Glu Trp Val Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala				
65		70		75 80
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn				
	85		90	95
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val				
	100		105	110
Tyr Tyr Cys Ala Arg Val Leu Arg Phe Leu Glu Trp Leu Leu Tyr Tyr				
	115		120	125
Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr				
	130		135	140
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro				
145		150		155 160
Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val				
	165		170	175
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala				
	180		185	190
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly				
	195		200	205
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly				
	210		215	220
Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys				
225		230		235 240
Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys				
	245		250	255
Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys				
	260		265	270
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val				
	275		280	285
Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr				
	290		295	300
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu				





Gln Asp Ile Arg Arg Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys  
 50 55 60

Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Arg Leu Gln Ser Gly Val  
 65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr  
 85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln  
 100 105 110

His Asn Asn Tyr Pro Arg Thr Phe Gly Gln Gly Thr Glu Val Glu Ile  
 115 120 125

Ile Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
 145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
 165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
 180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
 195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
 210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

<210> 52

<211> 236

<212> PRT

<213> Homo sapiens

<400> 52

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15

Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
 20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
           35                          40                          45  
 Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys  
       50                          55                          60  
 Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val  
       65                          70                          75                          80  
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr  
                           85                          90                          95  
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln  
                           100                          105                          110  
 His Asn Ser Tyr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
           115                          120                          125  
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
       130                          135                          140  
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
       145                          150                          155                          160  
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
                           165                          170                          175  
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
                           180                          185                          190  
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
           195                          200                          205  
 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
       210                          215                          220  
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
       225                          230                          235

<210> 53

<211> 326

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus

# Sequence

<220>

<221> modified\_base

<222> (289)

<223> a, c, t, g, other or unknown

<400> 5'

```
gacatccaga tgacccagty tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
wtcacttgcc gggcaagtca ggrcattaga mrtgatttag gctggtwtca gcagaaacca 120
gggaaagcyc ctaagcgct gatctatgct gcatccmrwt trcammgwgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcmg cctgcagcct 240
gaagattttg caacttatta ctgtytacar cataatarrrt ayckkybsns kttggcsrr 300
gggaccrags tggaratcaw acgaac 326
```

<210> 54

<211> 322

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
Sequence

<400> 54

```
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgyaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagy asctwtttaa attggtatca gcagaaacca 120
gggaaagccc ctaarctct gatcyatgyt gcatccagtt trcaargtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacartr cccayyhc ttcggcgga 300
gggaccaagg tggagatcaa ac 322
```

<210> 55

<211> 325

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
Sequence

<220>

<221> modified\_base

<222> (291)

<223> a, c, t, g, other or unknown

<400> 55  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgya gggccagtca gagtgttmgc rgcagstact tagcctggta ccagcagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtw ttactgtcag cagtatggta gytcacctcs nacgttcggc 300  
caagggaacca aggtggaaat caaac 325

<210> 56  
<211> 376  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus  
Sequence

<400> 56  
caggtgcagc tgggtggagtc tgggggaggc ttggtcaagc ctggaggggc cctgagactc 60  
tcctgtgcag cctctggatt cacyttcagt gactactaya tgagctggat ccgccaggct 120  
ccaggggaagg ggctggartg ggtttcatac attagtagta gtggtagtag cakakactac 180  
gcagactctg tgaagggccc attcaccatc tccagggaca acgccaagaa ctactgttat 240  
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgy gagagatgga 300  
gtggaaacta ctttttacta ctactactac ggtatggacg tctggggcca agggaccacg 360  
gtcaccgtct cctcag 376

<210> 57  
<211> 358  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus  
Sequence

<220>  
<221> modified\_base  
<222> (337)  
<223> a, c, t, g, other or unknown

<400> 57  
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctgggtg ctccatcagt arttactact ggagctggat ccggcagccc 120  
gccgggaagg gactggagtg gattgggcgt atctatacca gtgggagcmc caactacaac 180  
cctccctca agagtcgagt caccatgtca gtagacacgt ccaagaacca gttctccctg 240  
aagctgarct ctgtgaccgc cgcggacacg gccgtgtatt actgtgcggt aacgattttt 300

ggagtgggta ttatctttga ctactggggc cagrganccc tggtcaccgt ctctcag 358

<210> 58

<211> 418

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
Sequence

<400> 58

caggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60  
tcctgtrcag cctctggatt caccttttagc agctatgcca tgarctgggt ccgccaggct 120  
ccagggaagg ggctggagtg ggtctcagst attastggka gtggtggtab yacatwctac 180  
gcagactccg tgaagggccc gttcaccatc tccagagaca attccargam cacgctgtat 240  
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagatctk 300  
ggctrsksyg actyttacta ctactactac ggtatggacg tctggggcca agggacyacg 360  
gtgattatga gttggttcga cccctggggc cagggaaccc tggtcaccgt ctctcag 418

<210> 59

<211> 364

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
Sequence

<400> 59

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctggtgg ctccatcagt agttactact ggagytggat ccggcagccc 120  
ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180  
ccctccctca agagtcgact caccatatca gtagacacgt ccaagaacca gttctccctg 240  
aagctgagyt ctgtgaccgc tgcggacacg gccgtgtatt actgtgccag gacgtatagc 300  
agttcgttct actactacgg tatggacgtc tggggccaag ggaccacggt caccgtctcc 360  
tcag 364

<210> 60

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gly-Ser Linker

<400> 60

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15